

## SEQUENCE LISTING

<110> Spiegelman, Bruce  
Yoon, Cliff

<120> Methods and Compositions for Modulating Gluconeogenesis  
Using PGC-1

<130> DFN-038

<140>

<141>

<150> 60/266,765

<151> 2001-02-05

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 3066

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (92)..(2482)

<400> 1

```

aattcggcac gaggttgccct gcatgagtgt gtgctgtgtg tcagagtgga ttggagttga 60
aaaagcttga ctggcgatcat tcgggagctg g atg gct tgg gac atg tgc agc      112
                               Met Ala Trp Asp Met Cys Ser
                               1               5

caa gac tct gta tgg agt gac ata gag tgt gct gct ctg gtt ggt gag      160
Gln Asp Ser Val Trp Ser Asp Ile Glu Cys Ala Ala Leu Val Gly Glu
          10               15               20

gac cag cct ctt tgc cca gat ctt cct gaa ctt gac ctt tct gaa ctt      208
Asp Gln Pro Leu Cys Pro Asp Leu Pro Glu Leu Asp Leu Ser Glu Leu
          25               30               35

gat gtg aat gac ttg gat aca gac agc ttt ctg ggt gga ttg aag tgg      256
Asp Val Asn Asp Leu Asp Thr Asp Ser Phe Leu Gly Gly Leu Lys Trp
          40               45               50               55

tgt agc gac caa tcg gaa atc ata tcc aac cag tac aac aat gag cct      304
Cys Ser Asp Gln Ser Glu Ile Ile Ser Asn Gln Tyr Asn Asn Glu Pro
          60               65               70

gcg aac ata ttt gag aag ata gat gaa gag aat gag gca aac ttg cta      352
Ala Asn Ile Phe Glu Lys Ile Asp Glu Glu Asn Glu Ala Asn Leu Leu
          75               80               85

gcg gtc ctc aca gag aca ctg gac agt ctc ccc gtg gat gaa gac gga      400
Ala Val Leu Thr Glu Thr Leu Asp Ser Leu Pro Val Asp Glu Asp Gly
          90               95               100

```

ttg ccc tca ttt gat gca ctg aca gat gga gcc gtg acc act gac aac	448
Leu Pro Ser Phe Asp Ala Leu Thr Asp Gly Ala Val Thr Thr Asp Asn	
105 110 115	
gag gcc agt cct tcc tcc atg cct gac ggc acc cct ccc cct cag gag	496
Glu Ala Ser Pro Ser Ser Met Pro Asp Gly Thr Pro Pro Pro Gln Glu	
120 125 130 135	
gca gaa gag ccg tct cta ctt aag aag ctc tta ctg gca cca gcc aac	544
Ala Glu Glu Pro Ser Leu Leu Lys Lys Leu Leu Leu Ala Pro Ala Asn	
140 145 150	
act cag ctc agc tac aat gaa tgc agc ggt ctt agc act cag aac cat	592
Thr Gln Leu Ser Tyr Asn Glu Cys Ser Gly Leu Ser Thr Gln Asn His	
155 160 165	
gca gca aac cac acc cac agg atc aga aca aac cct gcc att gtt aag	640
Ala Ala Asn His Thr His Arg Ile Arg Thr Asn Pro Ala Ile Val Lys	
170 175 180	
acc gag aat tca tgg agc aat aaa gcg aag agc att tgt caa cag caa	688
Thr Glu Asn Ser Trp Ser Asn Lys Ala Lys Ser Ile Cys Gln Gln Gln	
185 190 195	
aag cca caa aga cgt ccc tgc tca gag ctt ctc aag tat ctg acc aca	736
Lys Pro Gln Arg Arg Pro Cys Ser Glu Leu Leu Lys Tyr Leu Thr Thr	
200 205 210 215	
aac gat gac cct cct cac acc aaa ccc aca gaa aac agg aac agc agc	784
Asn Asp Asp Pro Pro His Thr Lys Pro Thr Glu Asn Arg Asn Ser Ser	
220 225 230	
aga gac aaa tgt gct tcc aaa aag aag tcc cat aca caa ccg cag tcg	832
Arg Asp Lys Cys Ala Ser Lys Lys Lys Ser His Thr Gln Pro Gln Ser	
235 240 245	
caa cat gct caa gcc aaa cca aca act tta tct ctt cct ctg acc cca	880
Gln His Ala Gln Ala Lys Pro Thr Thr Leu Ser Leu Pro Leu Thr Pro	
250 255 260	
gag tca cca aat gac ccc aag ggt tcc cca ttt gag aac aag act att	928
Glu Ser Pro Asn Asp Pro Lys Gly Ser Pro Phe Glu Asn Lys Thr Ile	
265 270 275	
gag cga acc tta agt gtg gaa ctc tct gga act gca ggc cta act cct	976
Glu Arg Thr Leu Ser Val Glu Leu Ser Gly Thr Ala Gly Leu Thr Pro	
280 285 290 295	
ccc aca act cct cct cat aaa gcc aac caa gat aac cct ttc aag gct	1024
Pro Thr Thr Pro Pro His Lys Ala Asn Gln Asp Asn Pro Phe Lys Ala	
300 305 310	
tcg cca aag ctg aag ccc tct tgc aag acc gtg gtg cca ccg cca acc	1072
Ser Pro Lys Leu Lys Pro Ser Cys Lys Thr Val Val Pro Pro Pro Thr	
315 320 325	
aag agg gcc cgg tac agt gag tgt tct ggt acc caa ggc agc cac tcc	1120
Lys Arg Ala Arg Tyr Ser Glu Cys Ser Gly Thr Gln Gly Ser His Ser	
330 335 340	

acc aag aaa ggg ccc gag caa tct gag ttg tac gca caa ctc agc aag 1168  
 Thr Lys Lys Gly Pro Glu Gln Ser Glu Leu Tyr Ala Gln Leu Ser Lys  
 345 350 355

tcc tca ggg ctc agc cga gga cac gag gaa agg aag act aaa cgg ccc 1216  
 Ser Ser Gly Leu Ser Arg Gly His Glu Glu Arg Lys Thr Lys Arg Pro  
 360 365 370 375

agt ctc cgg ctg ttt ggt gac cat gac tac tgt cag tca ctc aat tcc 1264  
 Ser Leu Arg Leu Phe Gly Asp His Asp Tyr Cys Gln Ser Leu Asn Ser  
 380 385 390

aaa acg gat ata ctc att aac ata tca cag gag ctc caa gac tct aga 1312  
 Lys Thr Asp Ile Leu Ile Asn Ile Ser Gln Glu Leu Gln Asp Ser Arg  
 395 400 405

caa cta gac ttc aaa gat gcc tcc tgt gac tgg cag ggg cac atc tgt 1360  
 Gln Leu Asp Phe Lys Asp Ala Ser Cys Asp Trp Gln Gly His Ile Cys  
 410 415 420

tct tcc aca gat tca ggc cag tgc tac ctg aga gag act ttg gag gcc 1408  
 Ser Ser Thr Asp Ser Gly Gln Cys Tyr Leu Arg Glu Thr Leu Glu Ala  
 425 430 435

agc aag cag gtc tct cct tgc agc acc aga aaa cag ctc caa gac cag 1456  
 Ser Lys Gln Val Ser Pro Cys Ser Thr Arg Lys Gln Leu Gln Asp Gln  
 440 445 450 455

gaa atc cga gcg gag ctg aac aag cac ttc ggt cat ccc tgt caa gct 1504  
 Glu Ile Arg Ala Glu Leu Asn Lys His Phe Gly His Pro Cys Gln Ala  
 460 465 470

gtg ttt gac gac aaa tca gac aag acc agt gaa cta agg gat ggc gac 1552  
 Val Phe Asp Asp Lys Ser Asp Lys Thr Ser Glu Leu Arg Asp Gly Asp  
 475 480 485

ttc agt aat gaa caa ttc tcc aaa cta cct gtg ttt ata aat tca gga 1600  
 Phe Ser Asn Glu Gln Phe Ser Lys Leu Pro Val Phe Ile Asn Ser Gly  
 490 495 500

cta gcc atg gat ggc cta ttt gat gac agt gaa gat gaa agt gat aaa 1648  
 Leu Ala Met Asp Gly Leu Phe Asp Asp Ser Glu Asp Glu Ser Asp Lys  
 505 510 515

ctg agc tac cct tgg gat ggc acg cag ccc tat tca ttg ttc gat gtg 1696  
 Leu Ser Tyr Pro Trp Asp Gly Thr Gln Pro Tyr Ser Leu Phe Asp Val  
 520 525 530 535

tcg cct tct tgc tct tcc ttt aac tct ccg tgt cga gac tca gtg tca 1744  
 Ser Pro Ser Cys Ser Ser Phe Asn Ser Pro Cys Arg Asp Ser Val Ser  
 540 545 550

cca ccg aaa tcc tta ttt tct caa aga ccc caa agg atg cgc tct cgt 1792  
 Pro Pro Lys Ser Leu Phe Ser Gln Arg Pro Gln Arg Met Arg Ser Arg  
 555 560 565

tca aga tcc ttt tct cga cac agg tcg tgt tcc cga tca cca tat tcc 1840  
 Ser Arg Ser Phe Ser Arg His Arg Ser Cys Ser Arg Ser Pro Tyr Ser  
 570 575 580

agg tca aga tca agg tcc cca ggc agt aga tcc tct tca aga tcc tgt 1888  
 Arg Ser Arg Ser Arg Ser Pro Gly Ser Arg Ser Ser Ser Arg Ser Cys  
 585 590 595

tac tac tat gaa tca agc cac tac aga cac cgc aca cac cgc aat tct 1936  
 Tyr Tyr Tyr Glu Ser Ser His Tyr Arg His Arg Thr His Arg Asn Ser  
 600 605 610 615

ccc ttg tat gtg aga tca cgt tca agg tca ccc tac agc cgt agg ccc 1984  
 Pro Leu Tyr Val Arg Ser Arg Ser Arg Ser Pro Tyr Ser Arg Arg Pro  
 620 625 630

agg tac gac agc tat gaa gcc tat gag cac gaa agg ctc aag agg gat 2032  
 Arg Tyr Asp Ser Tyr Glu Ala Tyr Glu His Glu Arg Leu Lys Arg Asp  
 635 640 645

gaa tac cgc aaa gag cac gag aag cgg gag tct gaa agg gcc aaa cag 2080  
 Glu Tyr Arg Lys Glu His Glu Lys Arg Glu Ser Glu Arg Ala Lys Gln  
 650 655 660

aga gag agg cag aag cag aaa gca att gaa gag cgc cgt gtg att tac 2128  
 Arg Glu Arg Gln Lys Gln Lys Ala Ile Glu Glu Arg Arg Val Ile Tyr  
 665 670 675

gtt ggt aaa atc aga cct gac aca acg cgg aca gaa ttg aga gac cgc 2176  
 Val Gly Lys Ile Arg Pro Asp Thr Thr Arg Thr Glu Leu Arg Asp Arg  
 680 685 690 695

ttt gaa gtt ttt ggt gaa att gag gaa tgc acc gta aat ctg cgg gat 2224  
 Phe Glu Val Phe Gly Glu Ile Glu Glu Cys Thr Val Asn Leu Arg Asp  
 700 705 710

gat gga gac agc tat ggt ttc atc acc tac cgt tac acc tgt gac gct 2272  
 Asp Gly Asp Ser Tyr Gly Phe Ile Thr Tyr Arg Tyr Thr Cys Asp Ala  
 715 720 725

ttc gct gct ctt gag aat gga tat act tta cgc agg tcg aac gaa act 2320  
 Phe Ala Ala Leu Glu Asn Gly Tyr Thr Leu Arg Arg Ser Asn Glu Thr  
 730 735 740

gac ttc gag ctg tac ttt tgt gga cgg aag caa ttt ttc aag tct aac 2368  
 Asp Phe Glu Leu Tyr Phe Cys Gly Arg Lys Gln Phe Phe Lys Ser Asn  
 745 750 755

tat gca gac cta gat acc aac tca gac gat ttt gac cct gct tcc acc 2416  
 Tyr Ala Asp Leu Asp Thr Asn Ser Asp Asp Phe Asp Pro Ala Ser Thr  
 760 765 770 775

aag agc aag tat gac tct ctg gat ttt gat agt tta ctg aag gaa gct 2464  
 Lys Ser Lys Tyr Asp Ser Leu Asp Phe Asp Ser Leu Leu Lys Glu Ala  
 780 785 790

cag aga agc ttg cgc agg taacgtgttc ccaggctgag gaatgacaga 2512  
 Gln Arg Ser Leu Arg Arg  
 795

gagatgggtca atacctcatg ggacagcgtg tcctttccca agactcttgc aagtcatact 2572

taggaatttc tcctacttta cactctctgt acaaaaataa aacaaaacaa aacaacaata 2632

acaacaacaa caacaacaat aacaacaaca accataccag aacaagaaca acggtttaca 2692

tgaacacagc tgctgaagag gcaagagaca gaatgataat ccagtaagca cacgtttatt 2752  
cacgggtgtc agctttgctt tccctggagg ctcttggtga cagtgtgtgt gcgtgtgtgt 2812  
gtgtgggtgt gcgtgtgtgt atgtgtgtgt gtgtacttgt ttggaaagta catatgtaca 2872  
catgtgagga cttgggggca cctgaacaga acgaacaagg gcgacccctt caaatggcag 2932  
catttccatg aagacacact taaaacctac aacttcaaaa tgttcgtatt ctatacaaaa 2992  
ggaaaaataaa taaatataaa aaaaaaaaaa aaaaaactcg agagatctat gaatcgtaga 3052  
tactgaaaaa cccc 3066

<210> 2  
<211> 797  
<212> PRT  
<213> Mus musculus

<400> 2  
Met Ala Trp Asp Met Cys Ser Gln Asp Ser Val Trp Ser Asp Ile Glu  
1 5 10 15  
Cys Ala Ala Leu Val Gly Glu Asp Gln Pro Leu Cys Pro Asp Leu Pro  
20 25 30  
Glu Leu Asp Leu Ser Glu Leu Asp Val Asn Asp Leu Asp Thr Asp Ser  
35 40 45  
Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile Ile Ser  
50 55 60  
Asn Gln Tyr Asn Asn Glu Pro Ala Asn Ile Phe Glu Lys Ile Asp Glu  
65 70 75 80  
Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu Asp Ser  
85 90 95  
Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu Thr Asp  
100 105 110  
Gly Ala Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met Pro Asp  
115 120 125  
Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu Lys Lys  
130 135 140  
Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu Cys Ser  
145 150 155 160  
Gly Leu Ser Thr Gln Asn His Ala Ala Asn His Thr His Arg Ile Arg  
165 170 175  
Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys Ala  
180 185 190  
Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser Glu  
195 200 205

- 6 -

Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys Pro  
 210 215 220  
 Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Ala Ser Lys Lys Lys  
 225 230 235 240  
 Ser His Thr Gln Pro Gln Ser Gln His Ala Gln Ala Lys Pro Thr Thr  
 245 250 255  
 Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly Ser  
 260 265 270  
 Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu Ser  
 275 280 285  
 Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala Asn  
 290 295 300  
 Gln Asp Asn Pro Phe Lys Ala Ser Pro Lys Leu Lys Pro Ser Cys Lys  
 305 310 315 320  
 Thr Val Val Pro Pro Pro Thr Lys Arg Ala Arg Tyr Ser Glu Cys Ser  
 325 330 335  
 Gly Thr Gln Gly Ser His Ser Thr Lys Lys Gly Pro Glu Gln Ser Glu  
 340 345 350  
 Leu Tyr Ala Gln Leu Ser Lys Ser Ser Gly Leu Ser Arg Gly His Glu  
 355 360 365  
 Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His Asp  
 370 375 380  
 Tyr Cys Gln Ser Leu Asn Ser Lys Thr Asp Ile Leu Ile Asn Ile Ser  
 385 390 395 400  
 Gln Glu Leu Gln Asp Ser Arg Gln Leu Asp Phe Lys Asp Ala Ser Cys  
 405 410 415  
 Asp Trp Gln Gly His Ile Cys Ser Ser Thr Asp Ser Gly Gln Cys Tyr  
 420 425 430  
 Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser Thr  
 435 440 445  
 Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys His  
 450 455 460  
 Phe Gly His Pro Cys Gln Ala Val Phe Asp Asp Lys Ser Asp Lys Thr  
 465 470 475 480  
 Ser Glu Leu Arg Asp Gly Asp Phe Ser Asn Glu Gln Phe Ser Lys Leu  
 485 490 495  
 Pro Val Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp Asp  
 500 505 510  
 Ser Glu Asp Glu Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr Gln  
 515 520 525

- 7 -

Pro Tyr Ser Leu Phe Asp Val Ser Pro Ser Cys Ser Ser Phe Asn Ser  
530 535 540

Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln Arg  
545 550 555 560

Pro Gln Arg Met Arg Ser Arg Ser Arg Ser Phe Ser Arg His Arg Ser  
565 570 575

Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly Ser  
580 585 590

Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr Arg  
595 600 605

His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser Arg  
610 615 620

Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Ala Tyr Glu  
625 630 635 640

His Glu Arg Leu Lys Arg Asp Glu Tyr Arg Lys Glu His Glu Lys Arg  
645 650 655

Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Lys Gln Lys Ala Ile  
660 665 670

Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr Thr  
675 680 685

Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu Glu  
690 695 700

Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile Thr  
705 710 715 720

Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr Thr  
725 730 735

Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly Arg  
740 745 750

Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Thr Asn Ser Asp  
755 760 765

Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp Phe  
770 775 780

Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg  
785 790 795

<210> 3

<211> 5

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> 2, 3

<223> Xaa = Any Amino Acid

<400> 3  
Leu Xaa Xaa Leu Leu  
1 5

<210> 4  
<211> 3023  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (89)..(2482)

<400> 4  
caggtggctg gttgcctgca tgagtgtgtg ctctgtgtca ctgtggattg gagttgaaaa 60  
agcttgactg gcgtcattca ggagctgg atg gcg tgg gac atg tgc aac cag 112  
Met Ala Trp Asp Met Cys Asn Gln  
1 5  
gac tct gag tct gta tgg agt gac atc gag tgt gct gct ctg gtt ggt 160  
Asp Ser Glu Ser Val Trp Ser Asp Ile Glu Cys Ala Ala Leu Val Gly  
10 15 20  
gaa gac cag cct ctt tgc cca gat ctt cct gaa ctt gat ctt tct gaa 208  
Glu Asp Gln Pro Leu Cys Pro Asp Leu Pro Glu Leu Asp Leu Ser Glu  
25 30 35 40  
cta gat gtg aac gac ttg gat aca gac agc ttt ctg ggt gga ctc aag 256  
Leu Asp Val Asn Asp Leu Asp Thr Asp Ser Phe Leu Gly Gly Leu Lys  
45 50 55  
tgg tgc agt gac caa tca gaa ata ata tcc aat cag tac aac aat gag 304  
Trp Cys Ser Asp Gln Ser Glu Ile Ile Ser Asn Gln Tyr Asn Asn Glu  
60 65 70  
cct tca aac ata ttt gag aag ata gat gaa gag aat gag gca aac ttg 352  
Pro Ser Asn Ile Phe Glu Lys Ile Asp Glu Glu Asn Glu Ala Asn Leu  
75 80 85  
cta gca gtc ctc aca gag aca cta gac agt ctc cct gtg gat gaa gac 400  
Leu Ala Val Leu Thr Glu Thr Leu Asp Ser Leu Pro Val Asp Glu Asp  
90 95 100  
gga ttg ccc tca ttt gat gcg ctg aca gat gga gac gtg acc act gac 448  
Gly Leu Pro Ser Phe Asp Ala Leu Thr Asp Gly Asp Val Thr Thr Asp  
105 110 115 120  
aat gag gct agt cct tcc tcc atg cct gac ggc acc cct cca ccc cag 496  
Asn Glu Ala Ser Pro Ser Ser Met Pro Asp Gly Thr Pro Pro Pro Gln  
125 130 135  
gag gca gaa gag ccg tct cta ctt aag aag ctc tta ctg gca cca gcc 544  
Glu Ala Glu Glu Pro Ser Leu Leu Lys Lys Leu Leu Leu Ala Pro Ala  
140 145 150  
aac act cag cta agt tat aat gaa tgc agt ggt ctc agt acc cag aac 592  
Asn Thr Gln Leu Ser Tyr Asn Glu Cys Ser Gly Leu Ser Thr Gln Asn  
155 160 165



cat gca aat cac aat cac agg atc aga aca aac cct gca att gtt aag	640
His Ala Asn His Asn His Arg Ile Arg Thr Asn Pro Ala Ile Val Lys	
170 175 180	
act gag aat tca tgg agc aat aaa gcg aag agt att tgt caa cag caa	688
Thr Glu Asn Ser Trp Ser Asn Lys Ala Lys Ser Ile Cys Gln Gln Gln	
185 190 195 200	
aag cca caa aga cgt ccc tgc tcg gag ctt ctc aaa tat ctg acc aca	736
Lys Pro Gln Arg Arg Pro Cys Ser Glu Leu Leu Lys Tyr Leu Thr Thr	
205 210 215	
aac gat gac cct cct cac acc aaa ccc aca gag aac aga aac agc agc	784
Asn Asp Asp Pro Pro His Thr Lys Pro Thr Glu Asn Arg Asn Ser Ser	
220 225 230	
aga gac aaa tgc acc tcc aaa aag aag tcc cac aca cag tcg cag tca	832
Arg Asp Lys Cys Thr Ser Lys Lys Lys Ser His Thr Gln Ser Gln Ser	
235 240 245	
caa cac tta caa gcc aaa cca aca act tta tct ctt cct ctg acc cca	880
Gln His Leu Gln Ala Lys Pro Thr Thr Leu Ser Leu Pro Leu Thr Pro	
250 255 260	
gag tca cca aat gac ccc aag ggt tcc cca ttt gag aac aag act att	928
Glu Ser Pro Asn Asp Pro Lys Gly Ser Pro Phe Glu Asn Lys Thr Ile	
265 270 275 280	
gaa cgc acc tta agt gtg gaa ctc tct gga act gca ggc cta act cca	976
Glu Arg Thr Leu Ser Val Glu Leu Ser Gly Thr Ala Gly Leu Thr Pro	
285 290 295	
ccc acc act cct cct cat aaa gcc aac caa gat aac cct ttt agg gct	1024
Pro Thr Thr Pro Pro His Lys Ala Asn Gln Asp Asn Pro Phe Arg Ala	
300 305 310	
tct cca aag ctg aag tcc tct tgc aag act gtg gtg cca cca cca tca	1072
Ser Pro Lys Leu Lys Ser Ser Cys Lys Thr Val Val Pro Pro Pro Ser	
315 320 325	
aag aag ccc agg tac agt gag tct tct ggt aca caa ggc aat aac tcc	1120
Lys Lys Pro Arg Tyr Ser Glu Ser Ser Gly Thr Gln Gly Asn Asn Ser	
330 335 340	
acc aag aaa ggg ccg gag caa tcc gag ttg tat gca caa ctc agc aag	1168
Thr Lys Lys Gly Pro Glu Gln Ser Glu Leu Tyr Ala Gln Leu Ser Lys	
345 350 355 360	
tcc tca gtc ctc act ggt gga cac gag gaa agg aag acc aag cgg ccc	1216
Ser Ser Val Leu Thr Gly Gly His Glu Glu Arg Lys Thr Lys Arg Pro	
365 370 375	
agt ctg cgg ctg ttt ggt gac cat gac tat tgc cag tca att aat tcc	1264
Ser Leu Arg Leu Phe Gly Asp His Asp Tyr Cys Gln Ser Ile Asn Ser	
380 385 390	
aaa acg gaa ata ctc att aat ata tca cag gag ctc caa gac tct aga	1312
Lys Thr Glu Ile Leu Ile Asn Ile Ser Gln Glu Leu Gln Asp Ser Arg	
395 400 405	

- 10 -

caa cta gaa aat aaa gat gtc tcc tct gat tgg cag ggg cag att tgt	1360
Gln Leu Glu Asn Lys Asp Val Ser Ser Asp Trp Gln Gly Gln Ile Cys	
410 415 420	
tct tcc aca gat tca gac cag tgc tac ctg aga gag act ttg gag gca	1408
Ser Ser Thr Asp Ser Asp Gln Cys Tyr Leu Arg Glu Thr Leu Glu Ala	
425 430 435 440	
agc aag cag gtc tct cct tgc agc aca aga aaa cag ctc caa gac cag	1456
Ser Lys Gln Val Ser Pro Cys Ser Thr Arg Lys Gln Leu Gln Asp Gln	
445 450 455	
gaa atc cga gcc gag ctg aac aag cac ttc ggt cat ccc agt caa gct	1504
Glu Ile Arg Ala Glu Leu Asn Lys His Phe Gly His Pro Ser Gln Ala	
460 465 470	
gtt ttt gac gac gaa gca gac aag acc ggt gaa ctg agg gac agt gat	1552
Val Phe Asp Asp Glu Ala Asp Lys Thr Gly Glu Leu Arg Asp Ser Asp	
475 480 485	
ttc agt aat gaa caa ttc tcc aaa cta cct atg ttt ata aat tca gga	1600
Phe Ser Asn Glu Gln Phe Ser Lys Leu Pro Met Phe Ile Asn Ser Gly	
490 495 500	
cta gcc atg gat ggc ctg ttt gat gac agc gaa gat aaa agt gat aaa	1648
Leu Ala Met Asp Gly Leu Phe Asp Asp Ser Glu Asp Lys Ser Asp Lys	
505 510 515 520	
ctg agc tac cct tgg gat ggc acg caa tcc tat tca ttg ttc aat gtg	1696
Leu Ser Tyr Pro Trp Asp Gly Thr Gln Ser Tyr Ser Leu Phe Asn Val	
525 530 535	
tct cct tct tgt tct tct ttt aac tct cca tgt aga gat tct gtg tca	1744
Ser Pro Ser Cys Ser Ser Phe Asn Ser Pro Cys Arg Asp Ser Val Ser	
540 545 550	
cca ccc aaa tcc tta ttt tct caa aga ccc caa agg atg cgc tct cgt	1792
Pro Pro Lys Ser Leu Phe Ser Gln Arg Pro Gln Arg Met Arg Ser Arg	
555 560 565	
tca agg tcc ttt tct cga cac agg tcg tgt tcc cga tca cca tat tcc	1840
Ser Arg Ser Phe Ser Arg His Arg Ser Cys Ser Arg Ser Pro Tyr Ser	
570 575 580	
agg tca aga tca agg tct cca ggc agt aga tcc tct tca aga tcc tgc	1888
Arg Ser Arg Ser Arg Ser Pro Gly Ser Arg Ser Ser Ser Arg Ser Cys	
585 590 595 600	
tat tac tat gag tca agc cac tac aga cac cgc acg cac cga aat tct	1936
Tyr Tyr Tyr Glu Ser Ser His Tyr Arg His Arg Thr His Arg Asn Ser	
605 610 615	
ccc ttg tat gtg aga tca cgt tca aga tcg ccc tac agc cgt cgg ccc	1984
Pro Leu Tyr Val Arg Ser Arg Ser Arg Ser Pro Tyr Ser Arg Arg Pro	
620 625 630	
agg tat gac agc tac gag gaa tat cag cac gag agg ctg aag agg gaa	2032
Arg Tyr Asp Ser Tyr Glu Glu Tyr Gln His Glu Arg Leu Lys Arg Glu	
635 640 645	

2025 RELEASE UNDER E.O. 14176

gaa Glu	tat Tyr	cgc Arg	aga Arg	gag Glu	tat Tyr	gag Glu	aag Lys	cga Arg	gag Glu	tct Ser	gag Glu	agg Arg	gcc Ala	aag Lys	caa Gln	2080										
650																655	660									
agg Arg	gag Glu	agg Arg	cag Gln	agg Arg	cag Gln	aag Lys	gca Ala	att Ile	gaa Glu	gag Glu	cgc Arg	cgt Arg	gtg Val	att Ile	tat Tyr	2128										
665																670	675			680						
gtc Val	ggg Gly	aaa Lys	atc Ile	aga Arg	cct Pro	gac Asp	aca Thr	aca Thr	cgg Arg	aca Thr	gaa Glu	ctg Leu	agg Arg	gac Asp	cgt Arg	2176										
685																690	695									
ttt Phe	gaa Glu	gtt Val	ttt Phe	ggg Gly	gaa Glu	att Ile	gag Glu	gag Glu	tgc Cys	aca Thr	gta Val	aat Asn	ctg Leu	cgg Arg	gat Asp	2224										
700																705	710									
gat Asp	gga Gly	gac Asp	agc Ser	tat Tyr	ggg Gly	ttc Phe	att Ile	acc Thr	tac Tyr	cgt Arg	tat Tyr	acc Thr	tgt Cys	gat Asp	gct Ala	2272										
715																720	725									
ttt Phe	gct Ala	gct Ala	ctt Leu	gaa Glu	aat Asn	gga Gly	tac Tyr	act Thr	ttg Leu	cgc Arg	agg Arg	tca Ser	aac Asn	gaa Glu	act Thr	2320										
730																735	740									
gac Asp	ttt Phe	gag Glu	ctg Leu	tac Tyr	ttt Phe	tgt Cys	gga Gly	cgc Arg	aag Lys	caa Gln	ttt Phe	ttc Phe	aag Lys	tct Ser	aac Asn	2368										
745																750	755			760						
tat Tyr	gca Ala	gac Asp	cta Leu	gat Asp	tca Ser	aac Asn	tca Ser	gat Asp	gac Asp	ttt Phe	gac Asp	cct Pro	gct Ala	tcc Ser	acc Thr	2416										
765																770	775									
aag Lys	agc Ser	aag Lys	tat Tyr	gac Asp	tct Ser	ctg Leu	gat Asp	ttt Phe	gat Asp	agt Ser	tta Leu	ctg Leu	aaa Lys	gaa Glu	gct Ala	2464										
780																785	790									
cag Gln	aga Arg	agc Ser	ttg Leu	cgc Arg	agg Arg	taacatgttc			cctagctgag			gatgacagag			2512											
795																										
ggatggcgaa																tacctcatgg		gacagcgcggt		ccttccttaa		agactattgc		aagtcatact		2572
taggaatttc																tcctacttta		cactctctgt		acaaaaacaa		aacaaaaacaa		caacaatata		2632
acaagaacaa																caacaacaat		aacaacaatg		gtttacatga		acacagctgc		tgaagaggca		2692
agagacagaa																tgatatccag		taagcacatg		tttattcatg		gggtgtcagct		ttgctttttcc		2752
tggagtctct																tgggtgatgga		gtgtgctgtgt		gtgcatgtat		gtgtgtgtgt		atgtatgtgt		2812
gtgggtgtgtg																tgcttggttt		aggggaagta		tgtgtgggta		catgtgagga		ctgggggcac		2872
ctgaccagaa																tgcgcaaggg		caaaccatth		caaatggcag		cagttccatg		aagacacact		2932
taaaacctag																aacttcaaaa		tgttcgtatt		ctattcaaaa		ggaaaaatat		atatatatat		2992
atatatatat																aaattaaaaa		aaaaaaaaaa		a						3023

- 12 -

<210> 5  
<211> 798  
<212> PRT  
<213> Homo sapiens

<400> 5  
Met Ala Trp Asp Met Cys Asn Gln Asp Ser Glu Ser Val Trp Ser Asp  
1 5 10 15  
Ile Glu Cys Ala Ala Leu Val Gly Glu Asp Gln Pro Leu Cys Pro Asp  
20 25 30  
Leu Pro Glu Leu Asp Leu Ser Glu Leu Asp Val Asn Asp Leu Asp Thr  
35 40 45  
Asp Ser Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile  
50 55 60  
Ile Ser Asn Gln Tyr Asn Asn Glu Pro Ser Asn Ile Phe Glu Lys Ile  
65 70 75 80  
Asp Glu Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu  
85 90 95  
Asp Ser Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu  
100 105 110  
Thr Asp Gly Asp Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met  
115 120 125  
Pro Asp Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu  
130 135 140  
Lys Lys Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu  
145 150 155 160  
Cys Ser Gly Leu Ser Thr Gln Asn His Ala Asn His Asn His Arg Ile  
165 170 175  
Arg Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys  
180 185 190  
Ala Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser  
195 200 205  
Glu Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys  
210 215 220  
Pro Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Thr Ser Lys Lys  
225 230 235 240  
Lys Ser His Thr Gln Ser Gln Ser Gln His Leu Gln Ala Lys Pro Thr  
245 250 255  
Thr Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly  
260 265 270  
Ser Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu  
275 280 285

Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala  
290 295 300

Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys  
305 310 315 320

Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser  
325 330 335

Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser  
340 345 350

Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His  
355 360 365

Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His  
370 375 380

Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile  
385 390 395 400

Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser  
405 410 415

Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys  
420 425 430

Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser  
435 440 445

Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys  
450 455 460

His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys  
465 470 475 480

Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys  
485 490 495

Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp  
500 505 510

Asp Ser Glu Asp Lys Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr  
515 520 525

Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn  
530 535 540

Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln  
545 550 555 560

Arg Pro Gln Arg Met Arg Ser Arg Ser Arg Ser Phe Ser Arg His Arg  
565 570 575

Ser Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly  
580 585 590

Ser Arg Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr  
595 600 605

Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser  
610 615 620

Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr  
625 630 635 640

Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys  
645 650 655

Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala  
660 665 670

Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr  
675 680 685

Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu  
690 695 700

Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile  
705 710 715 720

Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr  
725 730 735

Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly  
740 745 750

Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser  
755 760 765

Asp Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp  
770 775 780

Phe Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg  
785 790 795